

# **STIC Biotechnology Systems Branch**

## **RAW SEQUENCE LISTING ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 101535,414  
Source: PCT  
Date Processed by STIC: 5-27-05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.  
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:  
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE  
APPLICANT, WITH A NOTICE TO COMPLY or,  
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A  
NOTICE TO COMPLY  
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT  
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.  
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.  
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/535/414

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH-ALPHA HEADERS WHICH WERE INSERTED BY PTO SOFTWARE

1. Wrapped Nucleic The numbers at the end of each line "wrapped" down to the next line. This may occur if your file  
Wrapped Aminos was received in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2. Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3. Missigned Amino Numbering The numbering under each 5<sup>th</sup> amino acid is missigned. Do not use tab codes between numbers; use space characters, instead.

4. Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5. Variable Length Sequence(s) contains n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>,<223> section that some may be missing.

6. PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>,<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>,<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>,<223> sections for Artificial or Unknown sequences.

7. Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  
(i) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)  
(ii) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)  
(iii) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped

8. Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  
<210> sequence id number  
<400> sequence id number  
000

9. Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.

Per 1.823 of Sequence Rules, use of <220>,<223> is MANDATORY if n's or Xaa's are present.

In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10. Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence or scientific name (Genus/species). <220>,<223> section is required when <213> response is Unknown or Artificial Sequence.

11. Use of <220> Sequence(s) missing the <220> feature and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol 63, No 104, pp 29631-32) (Sec. 1.823 of Sequence Rules)

12. PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13. Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



PCT

**RAW SEQUENCE LISTING**  
 PATENT APPLICATION: US/10/535,414

DATE: 05/27/2005  
 TIME: 11:25:05

Input Set : A:\Q87920.ST25.txt  
 Output Set: N:\CRF4\05272005\J535414.raw

3 <110> APPLICANT: DiaGenic AS  
 5 <120> TITLE OF INVENTION: Diagnostic Probe kits  
 7 <130> FILE REFERENCE: Q87920  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/535,414  
 C--> 10 <141> CURRENT FILING DATE: 2005-05-19  
 12 <150> PRIOR APPLICATION NUMBER: GB 0227238.3  
 13 <151> PRIOR FILING DATE: 2002-11-21  
 15 <160> NUMBER OF SEQ ID NOS: 501  
 17 <170> SOFTWARE: PatentIn version 3.0  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 405  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: Homo sapiens  
 24 <220> FEATURE:  
 25 <221> NAME/KEY: misc\_feature  
 26 <222> LOCATION: ()..()  
 27 <223> OTHER INFORMATION: sequence 93  
 30 <400> SEQUENCE: 1  
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 35 gacctggcct agcagtttg ccctgctggc cttagcaggg agacagggga gcaaagaacg 180  
 37 ccaagccgga ggcccgaggc cagccggcct ctcgagagcc agagcagcag ttgaatgtaa 240  
 39 tgctggggac aggcatgctg cccggcgttag ggccgggacc cggacagacca ggtgactacc 300  
 41 agtcctgggg acacactcac cataaacaca tccccaggca ggacagatcg gggaaagggt 360  
 43 gtgtaccagg ctatgatttc tcttgcatta aaatgttata ttatt 405  
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 49 <213> ORGANISM: Homo sapiens  
 51 <220> FEATURE:  
 52 <221> NAME/KEY: misc\_feature ?  
 53 <222> LOCATION: ()..() - ?  
 54 <223> OTHER INFORMATION: sequence 108 - ?  
 57 <400> SEQUENCE: 2

Does Not Comply  
 Corrected Diskette Needed  
 (Pg. 1-5) 2

(Pg. 6-7)

See item #  
 9 on error  
1 summary  
 sheet.

W--> 60 ~~mac~~accatcatc aacaccttcc accaatactc tgtgaagctg gggcaccctg acaccctgaa 60  
 62 ccagggggaa ttcaaagagc tggcgcggaaa agatctgca aattttctca agaaggagaa 120  
 64 taagaatgaa aaggctcatag aacacatcat ggaggacctg gacacaaatg cagacaaagca 180  
 66 gctgagctc gaggagttca tcattgtat ggcggggcta acctgggctt cccacggaaa 240  
 68 gatgcacgag ggtgacgagg gcccggcca ccaccataag ccaggcctcg gggaggggcac 300  
 70 cccctaagac cacagtggcc aagatcacag tggccacggc cacggccaca gtcatggtgg 360  
 72 ccacggccac agccactaat caggaggcca ggccaccctg ccttaccca accaggccc 420  
 74 cggggcctgt tatgtcaaac tgtcttggct gtggggctag gggctggggc caaataaaagt 480  
 74 cggggcctgt tatgtcaaac tgtcttggct gtggggctag gggctggggc caaataaaagt 540

pls explain "N" locations →

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DATE: 05/27/2005  
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Input Set : A:\Q87920.ST25.txt  
Output Set: N:\CRF4\05272005\J535414.raw

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87	<223> OTHER INFORMATION: sequence 110	
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95	agtcaaggga atccccttat ttctgtttt catatgagga accctagagc agccaggtga	180
97	ggctctctag ttaataaaaa atcatggaaa gactctaatt gcagactctt cttaagtgtt	240
99	aatagggatt tttcagctt attttgggtg cagttccaa tttttaaaaa tggtgaggtt	300
101	atcttccca cttcccaaa cctaattctt gttagatgcatt tagtgttggaa ccaatgcattt	360
103	ctcatgtctc aatttttgt atatgcattt tttcagatg tattaaacaa acaaaaaccc	420
105	ttc	423
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109	<211> LENGTH: 286	
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114	<221> NAME/KEY: misc feature	
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116	<223> OTHER INFORMATION: sequence 192	
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124	gttaataaac caatttcagt ctcttggtt tgacagatgt accatggta tgtaagatgt	180
126	tgacctggg gtggctggg tgaagggtat acaggaactc tttgtactat ctctgcaact	240
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139	<223> OTHER INFORMATION: sequence 250	
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145	caggaaagac agggcgaccc ggaagtccaa ctacttcctt aagatcatcc aactattgg	120
147	tgattatccg aaatgtttca ttgtggggagc agacaatgtg ggctccaagc agatgcagca	180
149	gatccgcattc tcccttcgcg ggaaggctgt ggtgctgtg ggcaagaaca ccatgatgcg	240
151	caaggccatc cgagggcacc tggaaaacaa cccagctctg gagaaactgc tgccatcatat	300
153	ccggggaaat gtggctttg tggccacaa ggaggaccc actgagatca gggacatgtt	360
155	gctggccat aaggtgccag ctgctgcggc tgctgggtcc attgccccat gtgaagtac	420
157	tgtccagcc cagaacactg gtctcgcccg cgagaagacc tccttttcc aggctttagg	480

See item  
#9 on  
error  
summary  
sheet.

pls explain "N" locations.

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Input Set : A:\Q87920.ST25.txt  
Output Set: N:\CRF4\05272005\J535414.raw

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161	actgg						545
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165	<211>	LENGTH:	591				
166	<212>	TYPE:	DNA				
167	<213>	ORGANISM:	Homo sapiens				
169	<220>	FEATURE:					
170	<221>	NAME/KEY:	misc_feature	?			
171	<222>	LOCATION:	(...) ..()	?			
172	<223>	OTHER INFORMATION:	sequence 299				
175	<400>	SEQUENCE:	6				
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W--> 178	tttctttt	aaagatagag	attentacia	ctacttaaa	aatatagtca	ataaggtaact	120
180	aagatattgc	ttagcgtaa	gttttaacg	taattttat	agcttaagat	tttaagagaa	180
182	aatatgaaga	cttagaagag	tagcatgagg	aaggaaaaga	taaaaggttt	ctaaaacatg	240
184	acggaggtt	agatgaagct	tcttcatgga	gtaaaaaaatg	tattnaaag	aaaattgaga	300
186	gaaaggacta	cagagccccg	aattaatacc	aatagaaggg	caatgcttt	agattaaaat	360
188	gaaggtgact	taaacagctt	aaagtttagt	ttaaaaagttg	tagtgatttta	aaataatttg	420
190	aaggcgatct	ttaaaaaaga	gattaaaccg	aagggtgatta	aaagacctt	aaatccatga	480
192	cgcanggaga	attgcgcatt	taaagcctag	ttacgcattt	actaaacgca	gacgaaaatg	540
194	ggaagattaa	ttgggagtgg	taggtgaaa	caattttgga	gaagatagaa	g	591
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199	<212>	TYPE:	DNA				
200	<213>	ORGANISM:	Homo sapiens				
202	<220>	FEATURE:					
203	<221>	NAME/KEY:	misc_feature	?			
204	<222>	LOCATION:	(...) ..()	?			
205	<223>	OTHER INFORMATION:	sequence 300				
208	<400>	SEQUENCE:	7				
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211	ttccgagcat	tccagtaact	tttttgttga	tgtacttagc	tgtactataa	gtatgtggtt	120
213	tgtatgagat	gtttaaaaag	gccaaagata	aaaggtttct	tttttttcc	ttttttgtct	180
215	atgaagttgc	tgttatattt	tttggcctg	tttgatgtat	gtgtgaaaca	atgttgtcca	240
217	acaataaaca	ggaattttat	tttgctgagt	tgttctaaaa	aaaaaaaaaa	aaaaaaaaaa	297
220	<210>	SEQ ID NO:	8				
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222	<212>	TYPE:	DNA				
223	<213>	ORGANISM:	Homo sapiens	?			
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234	cggccacctc	ggcctcccga	aagtgcgtgg	attacaggcg	tgagccacgg	cgccccagccc	120
236	cagcctgtca	cttaaactga	taaacgacag	attaacagta	aaaaaatttt	attttgcata	180
238	cataatgagg	cttcacaaaa	gagaagtgaa	aacccaagta	ggagtttagg	gctggggct	240
240	tatataccat	ttaacaaggg	gtgataaaatt	gtaagagaat	ag		282

pls explain  
"N" locations.

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243 <210> SEQ ID NO: 9	
244 <211> LENGTH: 619	
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248 <220> FEATURE:	
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250 <222> LOCATION: (.) .( )	
251 <223> OTHER INFORMATION: sequence 304	
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257 gtaacaggtg ccattgttac tgtaactttt cacacatgcc tttagttga tgtcaaagtc	120
259 atcattttgt gttaaacagca agttatctgt taggctgcac atcatgaact ttacttttag	180
261 aaagtcttat ctttatgcc acagaaatag cattggcta tttagtcatgg atggcaaaga	240
263 aattaatttt gagttgtttg gataaaaatg tttcagttga ctgttagtgtg tattgagaga	300
265 cactgccagt aaacaaaactc tcttggtagg tggaaatccc ctagaagttt cagaaaattg	360
267 ggaggaggtg aacttaatta aataacttga attgtttaga catattcaga gcttcttatg	420
269 accttgaaga aatcacccaa cttcaaaaga cctcggttc ttcatgttta aaatttaggga	480
271 gtttgactag atgttaaat ctatgttta gtttaacttct aagatgtaaa aaccctcttg	540
273 tttaacaaaa acctacaaga tcaagttgct tatctgaaat ctttatgtaa caacactagt	600
275 cactaagtct agctcgacc	619
278 <210> SEQ ID NO: 10	
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280 <212> TYPE: DNA	
281 <213> ORGANISM: Homo sapiens	
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284 <221> NAME/KEY: misc feature	?
285 <222> LOCATION: (.) .( )	
286 <223> OTHER INFORMATION: sequence 306	
289 <400> SEQUENCE: 10	
290 cttttcctcc cgctgtcccc cacggagggg actgctctcc cccgctgcat cctttctgtg	60
292 aggtaccta cccaccttag cacctgagag ggtgaaatag aattcttaacc tcgacattcg	120
294 gaaagtgttt ttgagaagtc tcggtcgta agggaaatct tccaaatccg tgacgacta	180
296 acgtattggc acctgcctcc tcttcggcca ccccccagat gaggcagctg tgactgtgtc	240
298 aagggaaagcc acgactctga ccatagtctt ctctcagctt ccactgcccgt ctccacagga	300
300 aacccagaag ttctgtgaac aagtccatgc tgccatcaag gcatttattt cagtgtacta	360
302 tttgcttcca aaggatcagg ccctgagaac aatgacctt tttccttacaa cagtgtctgg	420
304 gttgcgtgcc agcagatgcc tcagataccat agagataaca aagctgcagc tcttttcatg	480
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311 <212> TYPE: DNA	
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323 tttaaaatggttt gggcagttt ttatgtttagt acatgttattt ctatcctact gatttatttg	120

pls explain "N" locations.

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Input Set : A:\Q87920.ST25.txt  
Output Set: N:\CRF4\05272005\J535414.raw

325	ctatatcatc taatttagtt tgaatattcc ataatttact taatttagtcc tgtatggaga	180
327	cctagctt ctcagtgtct actattataa acaatgctac agtgaatatt ggtataaaa	240
329	tccata <del>na</del> ccacgtacat atcttaagg <del>t</del> ctggaagaga tattgctaaa ccagaagata	300
331	acctgcattt aaaatttgac tgctagg <del>t</del> agg <del>tt</del> acat ttaattaaat tagacaacaa	360
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343	<222> LOCATION: (.) .( ) ?	
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350	taggcaatct gaaggaaacc agaaaatgtg aatttctt ccctcaaaaa gctatactga	120
352	agtagtattt aatattcaag tacttgtaaa tttcagaac agtactttt aatttgaccc	180
354	atgaattcta tttaaatttg tcacttaata tttagccaag aagcaa <del>cc</del> tctaaaaaga	240
356	tttctggttt atttctcaa ctcctaataa atagggtcac atatttttta actttttct	300
358	aatttggaaa gtaatacagg catatggat tttaaaaatg aaacaacaca aagggatatg	360
360	ttttgaaaag tggcttgcc atccctgaac tgtaatcatc ccta <del>acat</del> t <del>cata</del> cctgt	420
362	ttcattttt aaagtgggt cagttttt attag <del>t</del> acat gtatttctat cctactgatt	480
364	tatttctat atcat <del>t</del> at ttagttgaa tattccataa ttacttaat tagcctgt <del>a</del>	540
366	tggagaccta gctcttctca g <del>t</del> gtctacta ttataaacaa tgctac <del>at</del> g aatattgg <del>t</del>	600
W-->	368 <del>nataaattcct acacaccacg taacatatact taagttcctg gaagagat<del>at</del> tgctaaacca</del>	660
370	gaagataacc tgcattaaa atttgactgc tagg <del>gt</del> tcagg gtcacat <del>tta</del> aattaaatta	720
372	gaacaaggaa <del>g</del> tgcataatgt ct <del>c</del> tgat <del>ac</del> g aatctattca aggtgcac <del>cc</del> tgg <del>t</del> cacaaa	780
374	ggaaagcaaa actgtc	796
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378	<211> LENGTH: 564	
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384	<222> LOCATION: (.) .( ) ?	
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391	aatttctatg g <del>t</del> aaatagtc cttttcttag cttctgc <del>nn</del> tcacttgctt attttttgtg	120
393	tgg <del>aa</del> atggg gttggataaa ccaatgaact ttattataaa caaatcccac ctatata <del>ca</del>	180
395	caaatttata tttcgg <del>t</del> ga aatacagata tttgc <del>ttt</del> tc tggagta <del>t</del> tagaagctgt	240
397	caat <del>at</del> gtat ctactgtaca gtactaaata gtattcattt atgaaat <del>at</del> g tagt <del>ttt</del> gg	300
399	gtggctgggg ttaaggaaaa atgagacttg gaattgt <del>ac</del> ttttatccaa gttt <del>at</del> g <del>at</del> ta	360
401	taaata <del>gg</del> gt tttgtttgt ttttttaac ct <del>aaa</del> actg aaat <del>cc</del> ata tagaaaaaca	420
403	gcattgttt tacagt <del>tt</del> gt agtaagtaac ttttaaaga ttttat <del>ca</del> aaa aagaattttg	480
405	tctat <del>at</del> ga gtaaaaagaag ttctataat ggcctaatca ctgcattttt aaaaaacaaa	540
407	gttcaacaca aatgacattt gttt	564
410	<210> SEQ ID NO: 14	
411	<211> LENGTH: 230	

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

Same error

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/535,414

DATE: 05/27/2005  
TIME: 11:25:06

Input Set : A:\Q87920.ST25.txt  
Output Set: N:\CRF4\05272005\J535414.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; N Pos. 61,464  
Seq#:4; N Pos. 64,65  
Seq#:6; N Pos. 85,485  
Seq#:10; N Pos. 513,520,529  
Seq#:11; N Pos. 21,235,248,329,335,359,372  
Seq#:12; N Pos. 601  
Seq#:13; N Pos. 6,26,55,73,99,100,180,228,486  
Seq#:15; N Pos. 149,177,463  
Seq#:20; N Pos. 557  
Seq#:22; N Pos. 199  
Seq#:24; N Pos. 149,177,463  
Seq#:25; N Pos. 388,506,672  
Seq#:26; N Pos. 524  
Seq#:28; N Pos. 213,306  
Seq#:31; N Pos. 448,617,663,677,706,710  
Seq#:32; N Pos. 53,89  
Seq#:34; N Pos. 5,8,21,25,65,79,80,103,143,481  
Seq#:35; N Pos. 6  
Seq#:36; N Pos. 525  
Seq#:42; N Pos. 119,121,157,205,214,216,229,252,327,329,354,361  
Seq#:45; N Pos. 304  
Seq#:47; N Pos. 7  
Seq#:55; N Pos. 462  
Seq#:57; N Pos. 571  
Seq#:63; N Pos. 441  
Seq#:65; N Pos. 270,280,310,359  
Seq#:66; N Pos. 195,201  
Seq#:67; N Pos. 606  
Seq#:68; N Pos. 92,642  
Seq#:69; N Pos. 44  
Seq#:70; N Pos. 684,707,709,713,723,734,746,748  
Seq#:71; N Pos. 8  
Seq#:73; N Pos. 280,342,500  
Seq#:74; N Pos. 552  
Seq#:76; N Pos. 461,483,497  
Seq#:77; N Pos. 567,575  
Seq#:84; N Pos. 223,280,297,302,337  
Seq#:85; N Pos. 9,29,49,94,105,152,169  
Seq#:88; N Pos. 529,542,559  
Seq#:93; N Pos. 70,75,88,102,114,127,129  
Seq#:95; N Pos. 650,685  
Seq#:96; N Pos. 204,255  
Seq#:97; N Pos. 248,519  
Seq#:98; N Pos. 425

RAW SEQUENCE LISTING ERROR SUMMARY                   DATE: 05/27/2005  
PATENT APPLICATION: US/10/535,414                   TIME: 11:25:06

Input Set : A:\Q87920.ST25.txt  
Output Set: N:\CRF4\05272005\J535414.raw

Seq#:99; N Pos. 552  
Seq#:101; N Pos. 565,581  
Seq#:102; N Pos. 86,168,230,241,257,337,339  
Seq#:103; N Pos. 20,22,47,546,562,611,645  
Seq#:107; N Pos. 708  
Seq#:109; N Pos. 600  
Seq#:110; N Pos. 616,635

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/535,414

DATE: 05/27/2005

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Input Set : A:\Q87920.ST25.txt

Output Set: N:\CRF4\05272005\J535414.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:60 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:60  
M:341 Repeated in SeqNo=2  
L:122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:60  
L:178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:60  
M:341 Repeated in SeqNo=6  
L:306 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:480  
L:321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0  
M:341 Repeated in SeqNo=11  
L:368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:600  
L:389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0  
M:341 Repeated in SeqNo=13  
L:447 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:120  
M:341 Repeated in SeqNo=15  
L:610 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:540  
L:672 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:180  
L:742 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:120  
M:341 Repeated in SeqNo=24  
L:783 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:360  
M:341 Repeated in SeqNo=25  
L:824 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:480  
L:876 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:180  
M:341 Repeated in SeqNo=28  
L:991 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:420  
M:341 Repeated in SeqNo=31  
L:1016 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0  
M:341 Repeated in SeqNo=32  
L:1078 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0  
M:341 Repeated in SeqNo=34  
L:1113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:0  
L:1164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:480  
L:1296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:60  
M:341 Repeated in SeqNo=42  
L:1393 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:300  
L:1439 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47 after pos.:0  
L:1709 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:55 after pos.:420  
L:1777 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:57 after pos.:540  
L:1969 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63 after pos.:420  
L:2027 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65 after pos.:240  
M:341 Repeated in SeqNo=65  
L:2052 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66 after pos.:180  
L:2087 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67 after pos.:600  
L:2104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68 after pos.:60  
M:341 Repeated in SeqNo=68  
L:2137 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69 after pos.:0  
L:2194 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70 after pos.:660  
M:341 Repeated in SeqNo=70

**VERIFICATION SUMMARY**  
PATENT APPLICATION: US/10/535,414

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Input Set : A:\Q87920.ST25.txt  
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L:2211 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71 after pos.:0  
L:2265 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73 after pos.:240  
M:341 Repeated in SeqNo=73  
L:2306 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74 after pos.:540